Identification of acceptor substrate binding subsites+2 and+3 in the amylomaltase from Thermus thermophilus HB8

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Table S1. Sequences used for construction of Sequence Logos in Figure 3.

CGTase sequences

Accession #	**Organisms**
Q5ZEQ7	*Anaerobranca gottschalkii*
Q7X3T0	*Bacillus agaradhaerens*
P30920	*Bacillus circulans*
Q9F5W3	*Bacillus circulans*
P43379	*Bacillus circulans.*
Q8L3E0	*Bacillus clarkii*
P14014	*Bacillus licheneformis.*
P27036	*Bacillus ohbensis.*
Q59239	*Bacillus sp.*
O82984	*Bacillus sp.*
Q5U9V9	*Bacillus sp.* G1-2004
P05618	*Bacillus sp.* Strain 1011
P31746	*Bacillus sp*. Strain 1-1
P30921	*Bacillus sp.* Strain 17-1
P09121	*Bacillus sp.* Strain 38-2
P31747	*Bacillus sp.* Strain 6.6.3
P17692	*Bacillus sp.* Strain B1018
Q5U9W0	*Bacillus sp.* TS1-1
P31797	*Bacillus stearothermophilus*
Q9ZAQ0	*Bacillus stearothermophilus*
O30565	*Brevibacillus brevis*
P08704	*Klebsiella oxytoca*
Q8RMG0	*Nostoc sp.* Strain PCC 9229
P31835	*Paenibacillus macerans*
P04830	*Paenibacillus macerans*
Q8X268	*Pyrococcus kodakaraensis*
P26827	*Thermoanaerobacter thermosulfuregenes*
Q9UWN2	*Thermoscoccus sp.* B1001
Q1VFW4	*Vibrio alginolyticus* 12G01
Q87FT5	*Vibrio parahaemolyticus.*

α-amylase sequences

Accession #	**Organism**
P53354	*Aedes aegypti*
P22630	*Aeromonas hydrophila*
P00692	*Bacillus amyloliquefaciens*
P08137	*Bacillus circulans*
P06278	*Bacillus licheniformis*
P20845	*Bacillus megaterium*
P19571	*Bacillus sp.* Strain 707
P19531	*Bacillus stearothermophilus*
P06279	*Bacillus stearothermophilus*

P00691	*Bacillus subtilis*
Q08806	*Debaryomyces occidentalis*
P14899	*Dictyoglomus thermophilum*
Q23835	*Drosophila ananassae*
O18345	*Drosophila ananassae*
Q23834	*Drosophila ananassae*
Q9GQV3	*Drosophila jambulina*
P81641	*Drosophila melanogaster*
P08144	*Drosophila melanogaster*
O18408	*Drosophila melanogaster*
O18552	*Drosophila pseudoobscura*
O18420	*Drosophila subobscura*
Q9BN01	*Drosophila yakuba*
O76264	*Drosophila yakuba*
P19961	*Homo sapiens*
P04746	*Homo sapiens*
P04745	*Homo sapiens*
P04747	*Hordeum vulgare*
P00688	*Mus musculus*
P00687	*Muse musculus*
P27934	*Oriza sativa*
P17654	*Oryza sativa*
P27933	*Oryza sativa*
P91778	*Pecten maximus*
P22963	*Pseudomonas saccharophila*
P13507	*Pseudomonas stutzeri*
P00689	*Rattus norvegicus*
P56634	*Tenebrio molitor*

Amylomaltase sequences

Accession #	**Organism**
BA000019	*Anabaena* sp. (strain 7120)
AE000704	*Aquifex aeolicus* VF5
AC002409	*Arabidopsis thaliana*
AY037231	*Arabidopsis thaliana*
NCC2705	*Bifidobacterium longum*
AE014792	*Bifidobacterium longum*
AE014673	*Bifidobacterium longum* NCC2705
AE001127,	*Borrelia burgdorferi*
AE002303	*Chlamydia muridarum*
AE001283	*Chlamydia trachomatis* D/UW-3/CX
AF307842	*Chlamydomonas reinhardtii*
AE016995	*Chlamydophila caviae* GPIC

AE017158	*Chlamydophila pneumoniae* TW-183
L37874	*Clostridium butyricum* NCIMB 7423
AP005221	*Corynebacterium efficiens* YS-314
AX065283	*Corynebacterium glutamicum*
M32793	*Escherichia coli* K12
AE010594	*Fusobacterium nucleatum* subsp. *nucleatum* ATCC 25586
U32815	*Haemophilus influenzae* Rd
AE006302	*Lactococcus lactis* subsp. *lactis* IL1403
AL022021	*Mycobacterium tuberculosis* H37Rv
AP004009	*Oryza sativa*
AE006089	*Pasteurella multocida* PM70
AE004643	*Pseudomonas aeruginosa* PAO1
AE009809	*Pyrobaculum aerophilum IM2*
AL646077	*Ralstonia solanacearum* GMI1000
AE016847	*Salmonella enterica* subsp. *enterica serovar* Typhi Ty2
AE015595	*Shewanella oneidensis* MR-1
X68664	*Solanum tuberosum*
AE014257	*Streptococcus agalactiae* 2603V/R
AE014987	*Streptococcus mutans* UA159
J01796	*Streptococcus pneumoniae* TIGR4
AE006568	*Streptococcus pyogenes* M1 GAS SF370
AE010052	*Streptococcus pyogenes* MGAS8232
AL138662	*Streptomyces coelicolor* A3(2)
D90900	*Synechocystis* sp. PCC 6803
AP005371	*Thermosynechococcus elongatus* BP-1
AP008226	*Thermus thermophilus* HB8
AE004345	*Vibrio cholerae* N16961
AE011669	*Xanthomonas axonopodis* pv. *citri* str. 306
AE012138	*Xanthomonas campestris* pv. *campestris* str. ATCC 33913
AJ414141	*Yersinia pestis* CO92